Title: RB PATHWAY AND CHROMATIN REMODELING
GENES THAT ANTAGONIZE *LET-60* RAS SIGNALING
Applicant(s):Horvitz *et al.*
Filing Date: September 12, 2003
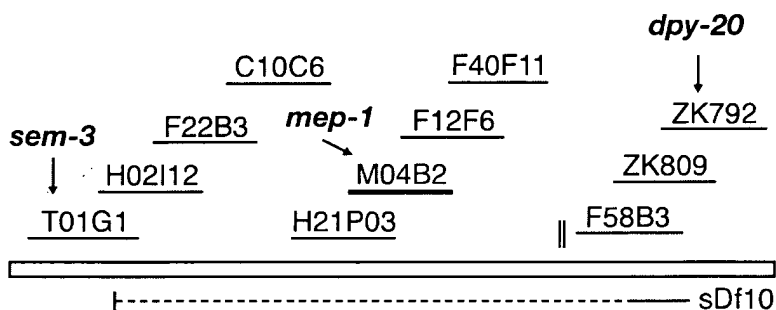Serial No. 10/661,398
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Fig. 1A

MVTADETVLATTTNTTSMSVEPTDPRSAGE 30

SSSDSEPDTIEQLKAEQREVMADAANGSEV 60

NGNQENGKEEAASADVEVIEIDDTEESTDP 90

SPDGSDENGDAASTSVPIEEEARKKDEGAS 120

EVTVASSEIEQDDDGDVMEITEEPNGKSED 130

TANGTVTEEVLDEEEPEPSVNGTTEIATEK 180

EPEDSSMPVEQNGKGVKRPVECIELDDDDD 210

DEIQEISTPAPAKKAKIDDVKATSVPEEDN 240

NEQAQKRLLDKLEEYVKEQKDQPSSKSRKV 270

LDTLLGAINAQVQKEPLSVRKLILDKVLVL 300

▾ n3680 S309N
PNTISFPPSQVCDLLIEHDPEMPLTKVINR 330

MFGEERPKLSDSEKRERAQLKQHNPVPNMT 360

KLLVDIGQDLVQEATYCDIVHAKNLPEVPK 390

NLETYKQVAAQLKPVWETLKRKNEPYKLKM 420

HR CDVCGFQTESKLVMSTHKENLH FTGSKF 450

▾ n3703 splice
Q CTMCKETDTSEQRMKDHYFETH LVIAKSE 480

EKESKYPCAICEEDFNFKGVREQHYKQCKK 510

DYIRIRNIMMPKQDDHLYINRWLWERPQLD 540

PSILQQQQQAALQQAQQKKQQQLLHQQQAA 570

QAAAAQLLRKQQLQQQQQQQQARLREQQQ 600

AAQFRQVAQLLQQQSAQAQRAQQNQGNVNH 630

NTLIAAMQASLRRGGQQGNSLAVSQLLQKQ 660

MAALKSQQGAQQLQAAVNSMRSQNSQKTPT 690

▾ n3702 Q706 amber
HRTPTFV CEICDASVQEKEKYLQHLQTTH K 720

QMVGKVLQDMSQGAPLA CSRCRDRFWTYEG 750

LERHLVMSH GLVTADLLLKAQKKEDGGR CK 780

TCGKNYAFNMLQHLVADH QVKLCSAEIMYS 810

CDVCAFKCSSYQTLEAHLTSNH PKGDKKTS 840

TPAKKDDCITLDD   853

Fig. 1B

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mep-1 genomic sequence
TCACACACTCATGACATACACACATCATTTCGCCTCACACACCGCGCCGTCGCCATCCGCACCG
CCCGGGTGGGACGTGTTCAAACTTTTCGGTTTTCGTAATTAATAGTGAGCCCCGGTTTATTCGC
TTTGAGAATCAGTATAATGGATATATCAGATTGTGTAATTAGGTTGCGTGCTTGAACTTTTAAA
ATTAACTGTTTTAAATTTATCTGCCTTTATCGTTACAGTAAATCATTTTGATGAACTTTTCGGA
TGAATCATAATGAAGTACGCAGCGCTCTAACAAAATGTGTTTGTAAATTCCAATTGCTACAAGT
TGCCCGGCTTATTTTTGGTGATTGAAGCATGATTCTGTTGACGCTCCCGACGCGGAATACCAG
GACGGACCGATGAGAGAGTACTGCCAGTGAAGAGACGCATGCGAGCAGGACGAGTGCTGCTCAC
CCTTCTTCTCAGCGTCGGCGGCTGCGACCAGCGGCCGAGGAAGGGGAGGAGAGAGGCCGATTTG
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GCTTGCCGCGCGCGCATTTTATTCCTACCAGTTTGAATCTCCCACCTCTCCGACTGTAACTG
TCCTAATTTGCTTCCTTCTCATCACTCTCTCTTTGCCTATTTCTCACTATCTAGACTCTATTTT
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TGGAACCAACGGATCCGAGAAGCGCTGGTGAATCGTCCTCAGATTCGGAGCCAGACACAATTGA
GGTGAGGAAAAGTTTTGGGAATTTAAATCTGAATAAAACGTTTTCAGCAGCTGAAGGCAGAACA
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CCTCACCTGATGGATCTGATGAAAACGGTGATGCTGCATCTACATCGGTTCCAATCGAAGAGGA
AGCGCGTAAAAAGGATGAGGGGGCTTCCGAAGTGACTGTGGCATCATCTGAGATTGAACAAGAC
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CAGAAGAGATTGCTCGACAAGCTGGAAGAGTATGTGAAGGAGCAGAAGGATCAACCATCCAGCA
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AGTCAAGTTTGCGACTTATTGATTGAGCACGATCCCGAAATGCCTTTGACGAAGGTTATCAACA
GGATGTTTGGAGAAGAAAGACCAAAGTTGAGTGATTCCGAGAAACGAGAGAGAGCTCAGCTGAA
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GAAGCTACCTATTGTGATATAGTTCACGCGAAGAATCTTCCAGAGGTGCCAAAAAATCTTGAAA
CCTATAAGCAAGTCGCTGCGCAGTTGAAACCAGTTTGGGAGACATTGAAACGCAAAAATGAGCC
GTACAAGTTGAAAATGCATCGATGCGACGTCTGTGGATTCCAGACGGAATCAAAGCTGGTTATG
AGCACTCACAAGGAGAATTTGCACTTCACAGGATCCAAATTCCAGTGCACCATGTGTAAAGAGA
CGGACACGAGTGAGCAAAGAATGAAGGATCACTACTTGTAAGTTTTTTTTTTTCATCTTTCAA
TATTCATTTAATTACAGCGAAACTCATCTTGTTATTGCAAAATCGGAAGAGAAGGAGTCCAAGT
ATCCATGTGCAATCTGCGAAGAAGACTTCAATTTCAAAGGTGTCCGTGAGCAGCATTACAAGCA
GTGCAAGAAGGACTACATTCGCATTCGAAACATCATGATGCCGAAGCAAGACGATCATCTCTAT
ATCAACAGATGGCTCTGGGAGAGGCCCCAATTGGATCCCAGCATTCTTCAACAGCAGCAACAAG
CTGCTCTTCAGCAAGCTCAACAAAGAAGCAACAGCAACTTCTGCATCAACAGCAAGCAGCACA
AGCTGCAGCCGCTGCGCAACTCTTACGGAAGCAACAATTACAACAGCAACAACAACAGCAACAG

Fig. 2A

Title: RB PATHWAY AND CHROMATIN REMODELING
GENES THAT ANTAGONIZE *LET-60* RAS SIGNALING
Applicant(s):Horvitz *et al.*
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```
GCTCGTCTTCGTGAGCAACAGCAAGCGGCCCAATTCCGGCAAGTGGCTCAACTGCTGCAACAAC
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GCTACTGTTGGCTCTTCTTCAGCTCCCACGTTTGTATGCGAAATTTGTGATGCGTCAGTGCAGG
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TTTTTTCAAAACCTAACTACCCCACAATTATCATGTAAAATCAAATTGCAATTCCCCATAAGAC
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TTTGTCCAGTTAAGATTTTTGGAAGATATCTAT
```

Fig. 2B

Title: RB PATHWAY AND CHROMATIN REMODELING
GENES THAT ANTAGONIZE *LET-60* RAS SIGNALING
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mep-1 ORF

```
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TGTCTGTGGAACCAACGGATCCGAGAAGCGCTGGTGAATCGTCCTCAGATTC
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GACGCGGCGAATGGTTCCGAAGTCAACGGAAATCAAGAGAACGGAAAAGAGG
AAGCGGCATCTGCAGACGTGGAAGTGATCGAGATAGATGACACCGAAGAGTC
TACGGATCCCTCACCTGATGGATCTGATGAAACGGTGATGCTGCATCTACA
TCGGTTCCAATCGAAGAGGAAGCGCGTAAAAAGGATGAGGGGGCTTCCGAAG
TGACTGTGGCATCATCTGAGATTGAACAAGACGATGATGGCGATGTTATGGA
AATCACTGAGGAGCCGAACGGAAAGTCGGAGGATACTGCCAACGGAACAGTT
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GATGATGACGAGATTCAGGAAATTTCTACCCCTGCCCCAGCTAAAAAAGCTA
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TCAATGCGCAAGTTCAAAAGGAGCCTCTGTCGGTTCGGAAGCTGATCCTGGA
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AGCTCAGCTGAAACAACATAATCCTGTTCCAAATATGACAAAACTGCTCGTG
GACATTGGACAGGATCTCGTTCAAGAAGCTACCTATTGTGATATAGTTCACG
CGAAGAATCTTCCAGAGGTGCCAAAAAATCTTGAAACCTATAAGCAAGTCGC
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TACTTCGAAACTCATCTTGTTATTGCAAAATCGGAAGAGAAGGAGTCCAAGT
ATCCATGTGCAATCTGCGAAGAAGACTTCAATTTCAAAGGTGTCCGTGAGCA
GCATTACAAGCAGTGCAAGAAGGACTACATTCGCATTCGAAACATCATGATG
CCGAAGCAAGACGATCATCTCTATATCAACAGATGGCTCTGGGAGAGGCCCC
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CAAGGAAATGTGAATCATAACACTCTGATTGCAGCAATGCAAGCGTCGTTGC
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```

Fig. 3A

Title: RB PATHWAY AND CHROMATIN REMODELING
GENES THAT ANTAGONIZE *LET-60* RAS SIGNALING
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CCACGTTTGTATGCGAAATTTGTGATGCGTCAGTGCAGGAAAAGGAGAAGT
ATCTACAGCATCTTCAGACTACTCATAAGCAGATGGTTGGAAAAGTGCTGC
AGGACATGTCGCAAGGAGCTCCACTGGCATGTTCTCGATGCCGTGACAGAT
TCTGGACTTATGAAGGGTTGGAGCGGCACTTGGTGATGTCGCATGGTCTCG
TCACTGCTGATCTGCTCCTCAAAGCGCAAAAGAAGGAAGACGGAGGTCGAT
GCAAGACATGCGGCAAGAACTATGCGTTCAACATGCTTCAACACTTGGTAG
CTGATCATCAAGTGAAGTTGTGCTCGGCTGAAATCATGTACTCGTGCGATG
TGTGCGCGTTCAAATGCTCGAGTTATCAGACTCTGGAAGCCCATCTCACTT
CAAATCACCCAAAAGGAGATAAGAAGACATCAACACCAGCAAAAAAGATG
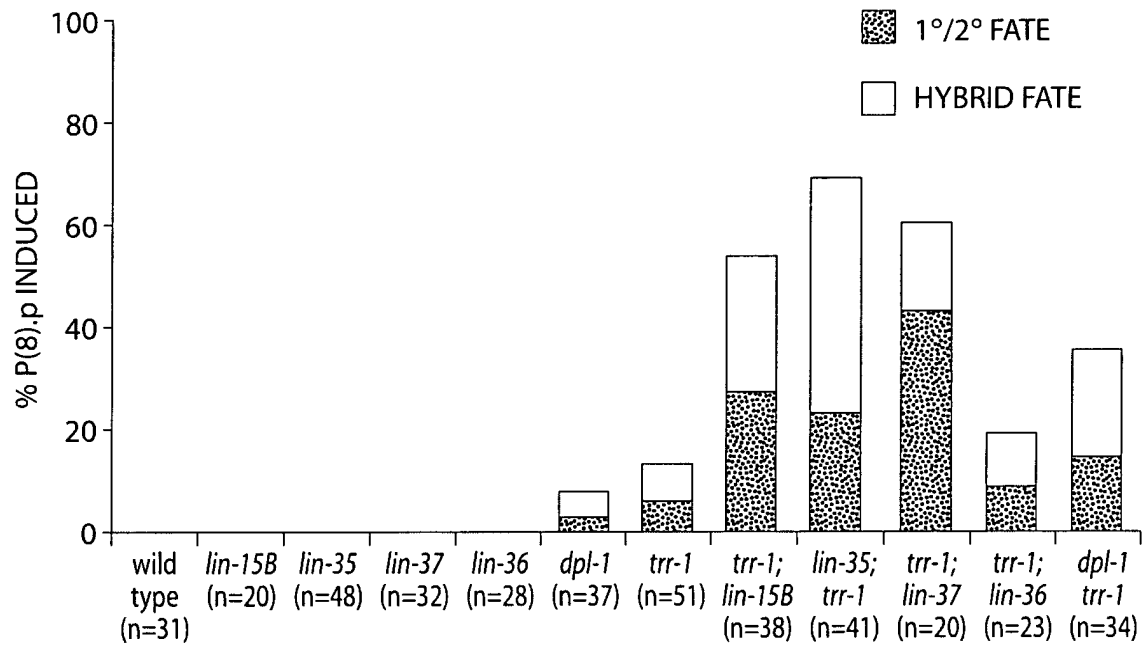ATTGTATTACTCTGGATGATTAA

Fig. 3B

Title: RB PATHWAY AND CHROMATIN REMODELING
GENES THAT ANTAGONIZE *LET-60* RAS SIGNALING
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Fig. 6

Title: RB PATHWAY AND CHROMATIN REMODELING
GENES THAT ANTAGONIZE *LET-60* RAS SIGNALING
Applicant(s):Horvitz *et al.*
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ssl-1 Genomic

```
cagctgatgt tgttgatgga aaaatgacgg ctgcaaagaa gccattggct gcaactgagc 60
caaaagtgca taataaataa atgtgtttct aggatcttct aataattttt tttctgtttt 120
ctagctctaa acttgtattt atttcattct tgttctacca aattcccacg gattctacgc 180
tttatgtttc taaattatta ttctttttta tttatatctg cattttcttc taaaaactct 240
ggtcattttc ttgtttttttt cttggtaatt ataaaaatta gtcatacaaa tcttgttaaa 300
tatctggcta ttcagtgaac aaaccatttt ccgctctaaa ttcgacccga atcaatcgaa 360
aaatggctca aaacgatgcc atctggctgc aacccccctg tcgtctctca attttgtgta 420
ctctctcgca gccacgcacg cgacgcaacg cactcgcgtc gcggtcgcag ttctttttca 480
aatttatcgc gccattttttg ttttgcctca tatttatcgg ctcacgattg attttcgtcg 540
aaaaacgcgc ttaatcgatt ccttttttacc tgaaaaatgt tgttccaatt ggaaaaccag 600
ttgaagatcg atgaattttc aagaaaatca ttcaaatagg caaaacccgc tgaactttga 660
aattcgattt ttgagttttt tgaagaaaat ataattattt catcatttat gttggtcctg 720
ttggtcctca gcatagaaaa ttcggacatg acattagaaa ttcataataa ctgctcccaa 780
tatcgggatt agaacgattt tcagctcaaa atatggaaaa ttggttacat aaaccgcata 840
tttgtagcat taatcttgaa cagctatatg gcattaaaaa aaaatatata tatacattgt 900
tttttctctc gaagtttctc tttttgtttc taaaatccgg aatataattt aaaaaaccac 960
ataaatttca atttgcagta cgagttcccc ccgaatcaca atg ccg gca aca ccg 1015
                                              Met Pro Ala Thr Pro
                                              1                 5
```

```
gtg cgt gct tca agt act cga ata agc aga cgt aca tca tca aga tca    1063
Val Arg Ala Ser Ser Thr Arg Ile Ser Arg Arg Thr Ser Ser Arg Ser
            10              15                  20
```

```
gtg gct gat gat cag cca tca act tcg tct gcg gtg gct cca cct cct    1111
Val Ala Asp Asp Gln Pro Ser Thr Ser Ser Ala Val Ala Pro Pro Pro
            25              30                  35
```

```
tca ccc att gcc ata gaa act gat gaa gat gcg gta gtt gag gag gag    1159
Ser Pro Ile Ala Ile Glu Thr Asp Glu Asp Ala Val Val Glu Glu Glu
        40              45              50
```

```
aaa aag aag aaa aag aca tca gat gat ttg gaa att atc act cca aga    1207
Lys Lys Lys Lys Lys Thr Ser Asp Asp Leu Glu Ile Ile Thr Pro Arg
    55              60              65
```

```
act cca gtc gat cgg cga att ccc tac att tgc tcg att ctt ttg act    1255
Thr Pro Val Asp Arg Arg Ile Pro Tyr Ile Cys Ser Ile Leu Leu Thr
70              75              80              85
```

```
gaa aat cga tcg att cgc gat aaa tt gtacgatttt ttaaatttaa           1301
Glu Asn Arg Ser Ile Arg Asp Lys Leu
            90
```

```
ttactttcct caaatccgaa taattattag atcgcgcttc gcgtttctgc atccgcggta 1361
tttttgccttc ccactgaaaa tagcagattt atcgaatttt tagcttaaaa aaaaaatgtt 1421
ttttctgcat ttttcaaaca aaccttttgt aaaacagtga aaatcgaatt tcaaatgact 1481
aaaatgaatt tttttttttgt ccactggttg tggaatggtt tgaatttgaa gaaatcagcg 1541
ggatttttcg tattttctga atattttct attaaaaatc ggtttcaaac cattttttga 1601
cttttgaata gaaaaatatt gagaaaatac gaaaaatcca gctaacttcc agcttgttca 1661
aattcaaacc attccacaac cagtggacga aaaaagttca ttttagtcat ttgaaattcg 1721
atttggtttg tttgaaaaat gcaaaaaaaa aatatttttt aaagctaaaa atttgataaa 1781
tctgaaaaaa atctgctatt ttcagtggaa aggcaaaata ccgcgaagcg cagcaagcgc 1841
gctctaataa ttattccgct tcgagaagag cgtgtattat ttcattgtta catttcaaaa 1901
```

Fig. 19A

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GENES THAT ANTAGONIZE LET-60 RAS SIGNALING
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```
ttatgaatta atgtttttca g g gtt ctg agc agc ggt cca gtt cgt caa gaa 1953
                          Val Leu Ser Ser Gly Pro Val Arg Gln Glu
                          95                    100

gat cac gaa gaa cag att gct cga gct caa cgg ata cag cca gtt gtc   2001
Asp His Glu Glu Gln Ile Ala Arg Ala Gln Arg Ile Gln Pro Val Val
105             110             115             120

gat caa att caa cga gtc gag caa at gtatgtgaag ctgaaaaatt          2047
Asp Gln Ile Gln Arg Val Glu Gln Ile
                125

gcaccacaaa tcaattattc taatcttgtt ttacag c ata ctc aat ggt tca gtg 2102
                                          Ile Leu Asn Gly Ser Val
                                          130                 135

gaa gat att ctg aaa gat cct cga ttc gca gta atg gca gat ctc aca   2150
Glu Asp Ile Leu Lys Asp Pro Arg Phe Ala Val Met Ala Asp Leu Thr
                140             145             150

aaa gaa cca cca cca aca cct gca cct cct cct cca atc cag aag aca   2198
Lys Glu Pro Pro Pro Thr Pro Ala Pro Pro Pro Pro Ile Gln Lys Thr
            155             160             165

atg caa ccg att gag gtg aaa att gag gat tca gag ggc tca aat acg   2246
Met Gln Pro Ile Glu Val Lys Ile Glu Asp Ser Glu Gly Ser Asn Thr
            170             175             180

gct caa ccg agt gtt ctg ccc agt tgt gga gga gga gag acg aat gtg   2294
Ala Gln Pro Ser Val Leu Pro Ser Cys Gly Gly Gly Glu Thr Asn Val
        185             190             195

gaa aga gcc gcc aaa aga gtgagttttg aagatagatt ggtgtgtaaa          2342
Glu Arg Ala Ala Lys Arg
200             205

aaatgaatgt ttatatattc actgcaactt tttcctcacg agggacgagg aaaagtggtt 2402
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gcctgttttc tttcgttttt catcgatttt tttcgttttt tcttaataaa actgataaat 2522
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aagcagcggt gaaagtggtc aatgcaatat gatggattac gggaatacaa aacctaaact 2642
ttttctgaaa catgatacat acgctgctta aatgctgaga ctacctgatt tcataacga  2702
gaccgctgaa aaagttttga ggttttcaaa attcaaattt tttggtgaaa aagtcgagat 2762
tttcgcacaa aaagttgaat tctgaaaacc tcaaattttt ttcagcggtc tcgttatgaa 2822
aatcaggtaa tttcagcatc atatgtatca tgtttcaaaa aaagtttagg ttttgtattc 2882
ccgtaatcca tcatattgca ttgaccactt tcaccgctgc ttgcccactg aatacatgat 2942
tttttacttg gaaattgttt tagcatctgc aaaaaatatt tatttatcag ttttattaag 3002
aaaaaacgaa aaaatcggt gaaaaacgaa agaaacagg cggaaaacaa agcaagataa   3062
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aatttcaacg ctcgctaata ttcctaattt gaaccgcgct tttgtccgcg ccgcactctg 3422
tagaattgca tccgcgctgt ttccttcctc ttccggcgcc ctacttcttt tcgattggaa 3482
```

Fig. 19B

Title: RB PATHWAY AND CHROMATIN REMODELING
GENES THAT ANTAGONIZE LET-60 RAS SIGNALING
Applicant(s):Horvitz et al.
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```
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gaatattagc gagagttgaa atttcaacaa aatcagccgc attttttttca aacttaatgt 3662
attttttttc gttttttcttt tgtagtaatt cggcatttgg ggctagtgta agcattttaa 3722
agtaaaatcc tcattttccg aactccacct ttaaaggtgg agtaccgaaa tttgagactt 3782
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                                          Glu Ala His Val Leu Ala
                                                              210
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```
cga atc gcc gag ctc cgt aag aac ggc tta tgg tcg aac agt cgt ctg   4485
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            215                 220                 225
```

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            230                 235                 240
```

```
ctg gaa gag gtc aaa tgg atg gca gtt gat ttc cga acc gag acg aat   4581
Leu Glu Glu Val Lys Trp Met Ala Val Asp Phe Arg Thr Glu Thr Asn
            245                 250                 255
```

```
acg aag cga aaa atc gcc aaa gtt ata gct cac gcc att gcg aaa cag   4629
Thr Lys Arg Lys Ile Ala Lys Val Ile Ala His Ala Ile Ala Lys Gln
260                 265                 270                 275
```

```
cac cgc gac aag cag atc gag att gag aga gcc gcc gaa cgg gag atc   4677
His Arg Asp Lys Gln Ile Glu Ile Glu Arg Ala Ala Glu Arg Glu Ile
                280                 285                 290
```

```
aag gag aag cga aaa atg tgt gca gga atc gcg aag atg gta cgg gat   4725
Lys Glu Lys Arg Lys Met Cys Ala Gly Ile Ala Lys Met Val Arg Asp
                295                 300                 305
```

```
ttc tgg tcg tct acg gat aaa gtt gtg gat att cga gcg aag gaa gtt   4773
Phe Trp Ser Ser Thr Asp Lys Val Val Asp Ile Arg Ala Lys Glu Val
            310                 315                 320
```

```
ctg gag tcg agg ctc agg aag gcg aga aat aag cat ttg atg ttt gta   4821
Leu Glu Ser Arg Leu Arg Lys Ala Arg Asn Lys His Leu Met Phe Val
            325                 330                 335
```

```
att gga caa gtc gat gaa atg agc aat att gtg caa gaa gga ctt gtt   4869
Ile Gly Gln Val Asp Glu Met Ser Asn Ile Val Gln Glu Gly Leu Val
340                 345                 350                 355
```

```
tca tcg tcg aaa tcc cca tca att gca tcg gat cga gat gat aaa gat   4917
Ser Ser Ser Lys Ser Pro Ser Ile Ala Ser Asp Arg Asp Asp Lys Asp
            360                 365                 370
```

Fig. 19C

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```
gaa gaa ttc aaa gca cct ggc tct gat tca gaa tct gac gat gag cag   4965
Glu Glu Phe Lys Ala Pro Gly Ser Asp Ser Glu Ser Asp Asp Glu Gln
        375             380             385

aca att gca aac gcg gaa aag tca cag aaa aag gaa gat gtt cga cag   5013
Thr Ile Ala Asn Ala Glu Lys Ser Gln Lys Lys Glu Asp Val Arg Gln
        390             395             400

gaa gtt gat gct ctt caa aac gag gca act gtg gat atg gat gac ttt   5061
Glu Val Asp Ala Leu Gln Asn Glu Ala Thr Val Asp Met Asp Asp Phe
405             410             415

ttg tac act tta ccg ccg gaa tat ctg aag gct tat ggt ctg acg cag   5109
Leu Tyr Thr Leu Pro Pro Glu Tyr Leu Lys Ala Tyr Gly Leu Thr Gln
420             425             430             435

gag gat ttg gag gag atg aag cgc gag aaa ttg gag gag cag aag gct   5157
Glu Asp Leu Glu Glu Met Lys Arg Glu Lys Leu Glu Glu Gln Lys Ala
            440             445             450

cgg aag gaa gct tgt ggt gat aat gag gag aaa atg gag att gat gaa   5205
Arg Lys Glu Ala Cys Gly Asp Asn Glu Glu Lys Met Glu Ile Asp Glu
        455             460             465

gttcgtagga tgctcctaaa aaaattacct aaaaaaaatc gattttccct ggaaaaaatc 5265
ctctggaaat gacccgaaac gtcatggcgg ctcgaaattt tgaaaaaaaa aaccccccaa 5325
atttccagct aaaatctcaa attttattgc atattttggt agttcttttg ttgtccgagg 5385
tgcgtttttc agctgaaaat gtacctgaat ctgcaagtaa acgaccaata tatgcaataa 5445
atgatgataa ttaatttccg atactgaaat gtgggcgaaa tttgagattt cgactgaaaa 5505
cgtcttaaaa atcacccaaa acccggcttt accgcacgaa ggtttgaaga aaatggccaa 5565
tttttagcca aaatctcaaa tttcgtccac ttttcagtca gaaattagtt ttttgaaatt 5625
aattaacacc ttttattgca tattttcgtc gtttattcgt tgatcgaggt gcttttttcgg 5685
tcgatgggtg cacaaattcg gtaattgtgc atccatcggc tgaaaatgct ccagaatttg 5745
cgaatgaacg gtgaaaattt aagattttag attgaaataa gccgtttttt agagaaaatt 5805
ggtcgttttg agacattaaa ttcaatttaa atccctctt tattttcag agc cca tca 5863
                                            Ser Pro Ser
                                                    470

tca gat gct caa aag cct tcc acc tca agc tca gat ctc acc gcc gag   5911
Ser Asp Ala Gln Lys Pro Ser Thr Ser Ser Ser Asp Leu Thr Ala Glu
            475             480             485

cag ctt caa gat cca aca gct gaa gac ggc aac ggt gat ggt cat ggt   5959
Gln Leu Gln Asp Pro Thr Ala Glu Asp Gly Asn Gly Asp Gly His Gly
            490             495             500

gta ctt gaa aac gtg gat tac gtg aag ctc aac agt cag gat agt gat   6007
Val Leu Glu Asn Val Asp Tyr Val Lys Leu Asn Ser Gln Asp Ser Asp
        505             510             515

gaa cga caa caa gag ttg gcg aat atc gca gaa gaa gcg ctg aaa ttc   6055
Glu Arg Gln Gln Glu Leu Ala Asn Ile Ala Glu Glu Ala Leu Lys Phe
        520             525             530
```

Fig. 19D

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```
cag cca aaa gga tat aca ctt gag acg aca caa gtc aag acg ccc gta   6103
Gln Pro Lys Gly Tyr Thr Leu Glu Thr Thr Gln Val Lys Thr Pro Val
535             540         545             550

cca ttc ctg att cga gga caa ctg aga gaa tat caa atg gtt gga ttg   6151
Pro Phe Leu Ile Arg Gly Gln Leu Arg Glu Tyr Gln Met Val Gly Leu
                555             560             565

gat tgg atg gtt aca ctt tat gag aag aat ttg aat gga att ctt gcc   6199
Asp Trp Met Val Thr Leu Tyr Glu Lys Asn Leu Asn Gly Ile Leu Ala
            570             575             580

gac gag atg ggc ctg gga aag acg att caa acg att tcc ctg ctg gct   6247
Asp Glu Met Gly Leu Gly Lys Thr Ile Gln Thr Ile Ser Leu Leu Ala
        585             590             595

cat atg gct tgt agt gaa tcg att tgg gga cca cac ttg att gtt gtg   6295
His Met Ala Cys Ser Glu Ser Ile Trp Gly Pro His Leu Ile Val Val
    600             605             610

ccg acg tct gtc att ctg aat tgg gag atg gag ttc aag aaa tgg tgt   6343
Pro Thr Ser Val Ile Leu Asn Trp Glu Met Glu Phe Lys Lys Trp Cys
615             620             625             630

ccg gct ctg aag att ttg acg tat ttt ggt acg gcg aag gag cgt gcc   6391
Pro Ala Leu Lys Ile Leu Thr Tyr Phe Gly Thr Ala Lys Glu Arg Ala
                635             640             645

gag aag cgg aag gga tgg atg aag ccg aat tgt ttc cat gtg tgc atc   6439
Glu Lys Arg Lys Gly Trp Met Lys Pro Asn Cys Phe His Val Cys Ile
            650             655             660

aca tca tac aag acg gtt act caa gat att aga gct ttt aag cag agg   6487
Thr Ser Tyr Lys Thr Val Thr Gln Asp Ile Arg Ala Phe Lys Gln Arg
    665             670             675

gtgcgtagaa attttgaaga tttgcggcga atttggcgaa tttgcataat ttttttaaaa 6547
ccaattttac cgataattgc gaaatttttc aattttatac agtggtcgga aattgctata 6607
attagtataa ttttttgcaaa aattggtact tttttcgaaa ttttgaacca ccataaaaca 6667
ttttttgaaca attttttaaga ggtttaataa cgaaattcgt tcatttgaac acattttggc 6727
gatatgaatc gcccgaaaat gtccccaat agacctaatt tcttaacaaa aatttaaaaa 6787
aaaatggccc aaaattgtct caaaatttcg aaaaaaaaac cgtaatttca gctgaaatct 6847
caaaatttgc caaattttcc gtctcacgga gatcagaaaa agttttttgc attttttttgt 6907
ggtttatttt agcgttatttt cgttaattta gatacatttt agcccaattt ttgcaaaaat 6967
tatactaatt atagcaattt ctgacccctg acaaactttg aaattatcgg taaacttggt 7027
ataaatggtt ttttttccaaa tttttaaagc gatattaaag gtggagtacc acaatttgag 7087
gctttgtttt ttttttttgga cccaaattgg tccaaaacta ccgaatttcg taatgagacg 7147
ctctgaaaat ttctttctca aaaaaaaagt tacggcggtt caaagttcgc ggcaaaataa 7207
ggcccatttt cagctaaaat caaaattttt tcccaacttc tcggtgtctc aacgcctgga 7267
```

<div align="center">Fig. 19E</div>

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```
acctaatttt tatttattca tcacttttta ataaatattg tggtctttga ttgggctttt 7327
attcgttgat ttaagtacat ttatggtcag tggggcacaa aatgtaactt ttttttcccaa 7387
agaccataaa tgtactttaa tcaacgaata aacgcccaat caaagaccac aatatttatt 7447
taaaagtaat gaataaataa taattaggtt ccagacgttg cgacaccgag aagttggaaa 7507
atttttttat tttagctgaa taagggcctt attgtctcaa actttgaacc gccataactt 7567
ttttttgaga acgtctcgtt acgaaattcg gtagttttgg accaatttgg gtctaaaaaa 7627
acaaagtctc aaatttcttg ttagagattt tttaaaaatt gatatttttt ttttcag gcc 7687
                                                              Ala
```

```
tgg cag tac cta att ctc gat gaa gct caa aat atc aaa aac tgg aag  7735
Trp Gln Tyr Leu Ile Leu Asp Glu Ala Gln Asn Ile Lys Asn Trp Lys
680             685             690                 695

tcc caa cgt tgg cag gct ctt ctg aat gtc cgt gct cga cgt cgc ctt  7783
Ser Gln Arg Trp Gln Ala Leu Leu Asn Val Arg Ala Arg Arg Arg Leu
            700             705             710

ctc ctg acc gga act cca ctt cag aac tct cta atg gaa ctg tgg tcg  7831
Leu Leu Thr Gly Thr Pro Leu Gln Asn Ser Leu Met Glu Leu Trp Ser
                715             720             725

ttg atg cat ttt ttg atg cca aca ata ttc tca agt cat gat gat ttc  7879
Leu Met His Phe Leu Met Pro Thr Ile Phe Ser Ser His Asp Asp Phe
            730             735             740

aag gat tgg ttc tcg aat ccg ttg aca ggg atg atg gaa gga aat atg  7927
Lys Asp Trp Phe Ser Asn Pro Leu Thr Gly Met Met Glu Gly Asn Met
    745             750             755

gaa ttc aat gct cca cta atc gga cga ctt cac aaa gtg ctc cgt ccg  7975
Glu Phe Asn Ala Pro Leu Ile Gly Arg Leu His Lys Val Leu Arg Pro
760             765             770             775

ttt att ctg cgg cgg ctc aag aag gaa gtt gag aag cag ctg cca gag  8023
Phe Ile Leu Arg Arg Leu Lys Lys Glu Val Glu Lys Gln Leu Pro Glu
            780             785             790

aag act gag cat att gtg aat tgt tcg ttg tca aag cgg cag aga tac  8071
Lys Thr Glu His Ile Val Asn Cys Ser Leu Ser Lys Arg Gln Arg Tyr
            795             800             805

ctg tac gat gac ttt atg agt cgt aga tca aca aag gag aat cta aag  8119
Leu Tyr Asp Asp Phe Met Ser Arg Arg Ser Thr Lys Glu Asn Leu Lys
            810             815             820

tct gga aat atg atg tcg gtg ctc aac att gtg atg caa ctc cga aaa  8167
Ser Gly Asn Met Met Ser Val Leu Asn Ile Val Met Gln Leu Arg Lys
    825             830             835

tgt tgt aat cat ccg aat ctc ttc gag ccg cgg cca gtt gtt gct ccg  8215
Cys Cys Asn His Pro Asn Leu Phe Glu Pro Arg Pro Val Val Ala Pro
840             845             850             855
```

Fig. 19F

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```
ttc gtc gtt gag aag ctt cag ctc gat gtt ccg gct cgt ctc ttt gaa   8263
Phe Val Val Glu Lys Leu Gln Leu Asp Val Pro Ala Arg Leu Phe Glu
            860             865             870

att tcg cag caa gat ccc tcc tcc tcc tca gct agt caa att ccg gaa   8311
Ile Ser Gln Gln Asp Pro Ser Ser Ser Ser Ala Ser Gln Ile Pro Glu
            875             880             885

att ttc aat tta tcc aaa atc ggc tat caa tct tcc gtt cga tct gca   8359
Ile Phe Asn Leu Ser Lys Ile Gly Tyr Gln Ser Ser Val Arg Ser Ala
            890             895             900

aaa cca ctc atc gaa gag ctt gaa gca atg agc act tat ccg gag cca   8407
Lys Pro Leu Ile Glu Glu Leu Glu Ala Met Ser Thr Tyr Pro Glu Pro
    905             910             915

cga gca cca gaa gtt ggc gga ttt cgg ttc aat cgg acg gct ttt gtt   8455
Arg Ala Pro Glu Val Gly Gly Phe Arg Phe Asn Arg Thr Ala Phe Val
920             925             930             935

gca aag aat ccg cat acg gaa gag tcg gag gac gaa ggt gtt atg aga   8503
Ala Lys Asn Pro His Thr Glu Glu Ser Glu Asp Glu Gly Val Met Arg
            940             945             950

agt cgt gtt ctg gtgaattttt aggaaaattg agaaaatgat ctaattgttg   8555
Ser Arg Val Leu
            955
```

```
aatttttaa agaatttatg ggccacaagc cgatttgccg gaaattttga tttttggcga 8615
tttgccgaaa attttgattt ttggcgattt gccagaaatt ttgatttttg gcaattatcc 8675
gatttgccgg aaattttgat ttttggcgat ttgccagaaa tttttgattt tggcaattat 8735
ccgatttgcc ggaaattttg aattttggca attttccgat ttgccggaaa tttttgattt 8795
tggcaatttg ccgaattgcc ggaaattttg attttttggca atttgccgaa ttgccggaaa 8855
ttttgattttt tggggatttg ccggaaattt tgattttttgg caatttgcct atttgtcgga 8915
aattttgatt tttggcaatt tgccgatttg tcggaaattt tgattttttgg caatttgccg 8975
atttgccgga aattttgatt tttggcaatt ttccgatttg ccaaaaattt tgattttttgg 9035
cgatttgccg atttgccgga aaacatttt gtgagccaat tttctcgaaa tttgggcttc 9095
aatattttca aattattcca aatttttccac tgattccgaa tatctaagta aaaaaaaatt 9155
ccctgatttt atatttcagc ttaaaatcgc taattttcgc gtcagagacg acgtcatgtg 9215
tcgatttact ggattttttaa tctttgtcgg atgctaattt ccgttttttca acgagtttcc 9275
ttcatttcca tcggtttttg acgaagtttt ctttgaaaat atgttcttaa ggtcaattaa 9335
acgtttttatt atcaaaaaaa actagcaaaa ttggctttaa aaacacattt tcacagaaaa 9395
ctccgacaaa aaccgacgaa aatgaaggaa acccccgtt tgaaaacaga aattagcatc 9455
tgataaagat taaatcccg taaatcgaca catggcgtct ggcgtctctg cacgaaaag 9515
tcgcgatttt aagctgacat acaaaaaaag agggatatat tttttacga atttttcaca 9575
tagatattcg aaatcagggg ggaaaatttg gagaaatttg agaaaatttc tcagatttcg 9635
gattaaaaat attcaatttt tgtttttctta tattaaaaaa aaattaactt ttataatttt 9695
```

```
tcag cca aaa cca att aat gga aca gct caa cca ctt caa aat gga aat   9744
     Pro Lys Pro Ile Asn Gly Thr Ala Gln Pro Leu Gln Asn Gly Asn
               960             965             970

tca ata cca caa aat gct cca aat cgt cca caa act tca tgc att cgt   9792
Ser Ile Pro Gln Asn Ala Pro Asn Arg Pro Gln Thr Ser Cys Ile Arg
            975             980             985
```

Fig. 19G

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```
tca aaa acc gtc gta aat aca gtt cca ctg acc atc tcc acc gat cga    9840
Ser Lys Thr Val Val Asn Thr Val Pro Leu Thr Ile Ser Thr Asp Arg
        990                 995                 1000

agt ggt ttt cat ttt aat atg gcc aat gtt gga aga ggt gtt gtt cgt    9888
Ser Gly Phe His Phe Asn Met Ala Asn Val Gly Arg Gly Val Val Arg
        1005                1010                1015

ttg gat gat tca gca cgt atg agc cca ccg ctc aaa cgt cag aag ctc    9936
Leu Asp Asp Ser Ala Arg Met Ser Pro Pro Leu Lys Arg Gln Lys Leu
    1020                1025                1030

acc gga act gca acg aat tgg agt gat tat gtt ccg cga cac gtt gtt    9984
Thr Gly Thr Ala Thr Asn Trp Ser Asp Tyr Val Pro Arg His Val Val
1035                1040                1045                1050

gaa aag atg gaa gaa tcg aga aaa aac cag ctg gaa att gtt cga agg    10032
Glu Lys Met Glu Glu Ser Arg Lys Asn Gln Leu Glu Ile Val Arg Arg
                1055                1060                1065

cga ttt gag atg att cgt gct ccg att att cca ctg gaa atg gtt gcg    10080
Arg Phe Glu Met Ile Arg Ala Pro Ile Ile Pro Leu Glu Met Val Ala
            1070                1075                1080

ctg gtt cga gag gaa att att gca gaa ttt cca cgt ttg gct gtg gaa    10128
Leu Val Arg Glu Glu Ile Ile Ala Glu Phe Pro Arg Leu Ala Val Glu
        1085                1090                1095

gag gac gag gtt gtg cag gag agg ctt ttg gag tat tgc gag ttg ttg    10176
Glu Asp Glu Val Val Gln Glu Arg Leu Leu Glu Tyr Cys Glu Leu Leu
    1100                1105                1110

gtg caa aggtagaatt ttgaaaatta ttactttgct ttttttaaa ccaaaattgg    10232
Val Gln
1115

cccaaaacta ccgaatttcg taatgagaca ttctgaaagc ttctcaaaaa aaaagttttg   10292
gccgctcaaa gttcgggaaa ataaggccca ttttcagctg aaatcaaaat ttttttccaac   10352
ttctcggtgt cgcaacgtct ggaactaaaa ttttggaaaa cgagaaattt tccattttttt   10412
gcaagctgaa aaatcaaagt ttttttttcc tcaaaattgg acaaacaaaa aaattttttt   10472
ttgaaaattg atcgaaaaaa ttcaaaattt ctataatttt tcgatttttt aaataaaact   10532
ttcatcattt ttcttccaaa tttagttttc tcgattttaa ctttttttcaa aaaaaaattt   10592
tttaatacga aaaaaattca attttagctc taattctttt ttagacccaa attggtccaa   10652
aactaccgaa tttcgtaatg agacgttctg aacatttctc aaaaaaaagt tatgacggtt   10712
caaagttcgg caaaataagg cccatttttca tataaaatca aatttttttt ctaacttctc   10772
ggtgtcacaa cgtctggaac ttaatttttta tttaattatt acttttcaat aaatattgtg   10832
gtcttttatt aggcgtttat ttgttgattt aagtacattt atggtcaagt ggggcccaaa   10892
taaaagttac attttgtgcc cacatgacca taaatgtact taaatcaacg aataaacgcc   10952
taatcaaagg ccacaatatt tattaaaaag tgttgaataa ataaaaatta ggttccagac   11012
attgtgacac cgagaagtta aaaaaaattt tgattttagc tgaaaatggg ccttatttttg   11072
ctgaacttta aaccgctata actttttttt gagaaatttt cagaacgtct cattacgaaa   11132
ttcggtagtt ttggaccaat ttgggtctaa aaaagaatta gagctaaaat tgaattttct   11192
tcgtattaaa aatttttttt ttgaaaaaag taaaatcga gaaaactaaa tttggaagaa   11252
aaatgatgaa aatttttattt aaaaaatcga aaaattatag aaattttgat cgattttttc   11312
gatcaatttt caataaaaaa ttttttgttt gtccaattttt gaggaaaaaa aaaactttga   11372
```

Fig. 19H

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```
tttttcagct tacaaaaaat ggaaagtttc tcgttttcca attttttgat gtggattttt  11432
atgagaaaaa atatataatg tcacaaaaaa tagattatta tctaaaaatc gaaaaaatta  11492
aattttccag ttttcaggaa aaaaatcgtt aagaaattgt ttttccatta aaggtggagt  11552
accgaatttt gagacgctgc ttttttagac ccaaaatggt ccaaaactac cgaatttcgt  11612
aatgatacgc tctgaaaaat tttcaaaaaa aaagttgtga ccgctcaaag ttttggaaaa  11672
atggcatatt tttagctaaa atctcaaatt ttggcaactt atcggtgtcg cagcggttgg  11732
aacttaattt ttatttaatt gtcattcatt aatgcatgtt ttggcatttc attatgtgtt  11792
atttcgttga ttgagatgct ttttgtgcct gcatcgacca aaaaaccatc tcaatcaacg  11852
aaataacaca taataaaatg ccaaaatatg cattaaagga tgataatcaa ataaaaatta  11912
agtttcaacc gctgcgacac cgctaagttg ccaaaatttg agattttagc taaaaatggt  11972
ccatttttct aaaactttga gcggtcacaa ctttttttttt gagaaatttt cagagcgtct  12032
cattacgaaa attggtaggt tcggaccaat ttgggtctaa aaaagcagcg tctcaaaatt  12092
cggtacttca cctttaaagt tttcaattta aagtataaat tatccaatca aaaattgacg  12152
aaaaaatttt ttaaaaattt tttcttccga aaaaaaaatt aattttaatt tttgtt aga  12211
                                                                    Arg


ttc gga atg tac gtc gaa cca gtg ctg acc gat gct tgg cag tgt cgt   12259
Phe Gly Met Tyr Val Glu Pro Val Leu Thr Asp Ala Trp Gln Cys Arg
        1120             1125             1130

cca tca tcg tct ggt ctt cca tca tat att cgc aac aat tta tca aat   12307
Pro Ser Ser Ser Gly Leu Pro Ser Tyr Ile Arg Asn Asn Leu Ser Asn
        1135             1140             1145

atc gag ctg aat tct cgt tct ctt ctc ctc aac acc tcc act aat ttc   12355
Ile Glu Leu Asn Ser Arg Ser Leu Leu Leu Asn Thr Ser Thr Asn Phe
1150             1155             1160             1165

gat acc cga atg tcg atc tca cgt gct ctt caa ttc cca gaa ctc cgt   12403
Asp Thr Arg Met Ser Ile Ser Arg Ala Leu Gln Phe Pro Glu Leu Arg
        1170             1175             1180

ctg atc gag tac gat tgt gga aag ctt cag acg ttg gct gtt ctg ctt   12451
Leu Ile Glu Tyr Asp Cys Gly Lys Leu Gln Thr Leu Ala Val Leu Leu
        1185             1190             1195

cgt cag ttg tac ctg tac aag cac aga tgt ctg atc ttc acg caa atg   12499
Arg Gln Leu Tyr Leu Tyr Lys His Arg Cys Leu Ile Phe Thr Gln Met
        1200             1205             1210

tca aag atg ctc gac gtt ctg cag acc ttc ctt tct cat cac ggt tat   12547
Ser Lys Met Leu Asp Val Leu Gln Thr Phe Leu Ser His His Gly Tyr
        1215             1220             1225

cag tat ttc cgc ctc gac ggt acc act ggt gtc gaa caa aga cag gcg   12595
Gln Tyr Phe Arg Leu Asp Gly Thr Thr Gly Val Glu Gln Arg Gln Ala
1230             1235             1240             1245

atg atg gag cgg ttc aac gcg gat ccc aag gtg ttt tgc ttc att ctg   12643
Met Met Glu Arg Phe Asn Ala Asp Pro Lys Val Phe Cys Phe Ile Leu
        1250             1255             1260

tcg acg aga tcc ggt ggt gtt gga gtc aat cta acc ggt gct gac act   12691
Ser Thr Arg Ser Gly Gly Val Gly Val Asn Leu Thr Gly Ala Asp Thr
        1265             1270             1275
```

Fig. 19I

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```
gtg atc ttc tac gat tcg gat tgg aat ccg acg atg gat gct cag gct   12739
Val Ile Phe Tyr Asp Ser Asp Trp Asn Pro Thr Met Asp Ala Gln Ala
        1280            1285            1290

cag gat aga tgt cat cgt atc gga cag acg agg aat gtc tcg att tat   12787
Gln Asp Arg Cys His Arg Ile Gly Gln Thr Arg Asn Val Ser Ile Tyr
        1295            1300            1305

cga ttg att tcc gag cga aca att gag gag aat att ctg aga aag gca   12835
Arg Leu Ile Ser Glu Arg Thr Ile Glu Glu Asn Ile Leu Arg Lys Ala
1310            1315            1320            1325

aca cag aag cgg cga ctt gga gag ttg gca att gac gag gct ggc ttc   12883
Thr Gln Lys Arg Arg Leu Gly Glu Leu Ala Ile Asp Glu Ala Gly Phe
                1330            1335            1340

aca ccc gag ttc ttc aaa caa tct gac agt att cgg gat ctt ttt gat   12931
Thr Pro Glu Phe Phe Lys Gln Ser Asp Ser Ile Arg Asp Leu Phe Asp
            1345            1350            1355

gga gag aat gtg gaa gtg act gct gtg gca gat gtt gcg acg acg atg   12979
Gly Glu Asn Val Glu Val Thr Ala Val Ala Asp Val Ala Thr Thr Met
        1360            1365            1370

agc gag aaa gaa atg gag gtt gcg atg gca aag tgt gaa gat gaa gct   13027
Ser Glu Lys Glu Met Glu Val Ala Met Ala Lys Cys Glu Asp Glu Ala
        1375            1380            1385

gat gtg aat gcg gcg aag att gcg gtg gcc gag gcg aac gtt gat aat   13075
Asp Val Asn Ala Ala Lys Ile Ala Val Ala Glu Ala Asn Val Asp Asn
1390            1395            1400            1405

gcg gag ttt gat gag aaa tca ttg ccg ccg atg agc aat ttg caa gga   13123
Ala Glu Phe Asp Glu Lys Ser Leu Pro Pro Met Ser Asn Leu Gln Gly
            1410            1415            1420

gat gag gag gct gat gag aag tat atg gag ttg ata caa c aggtaaaatt   13173
Asp Glu Glu Ala Asp Glu Lys Tyr Met Glu Leu Ile Gln
            1425            1430

cggcggaaat cggaaatttt cccatttaga atatcaaatt ttgcccgatt gtgtcgtttt   13233
ttgatttttc gatttattcg atttgttttt gagggaaaat cggaaaaatg ttcagaaaat   13293
taaccataac atgtgatctt tttaaaatct tagcgcaaat gtcttctaaa aaataaagaa   13353
tgaccaaaaa ttttaagcta attttgaaa aaccaaagaa aaaatttaga ttttcgatg    13413
ttttccgaga caaaaagaca aaaacggaaa ttgtcgaaaa tgaatgaaat ttttaatttt   13473
tcagcaaaaa aaaaatagta cttaattta aaaatgtga tcatttcggt aggaaaatct   13533
ggaaaaatcg attttcaaac aaaaaaaaac cgagcctcta caatcttttt ttttcccgaa   13593
atctccagaa cttctcacaa taacaactat ataaatttca aaatttc ag ctc aaa     13648
                                                    Gln Leu Lys
                                                        1435

cca atc gaa cga tat gcc att aac ttt ctt gag aca cag tac aag cca   13696
Pro Ile Glu Arg Tyr Ala Ile Asn Phe Leu Glu Thr Gln Tyr Lys Pro
        1440            1445            1450
```

Fig. 19J

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```
gaa ttt gag gaa gaa tgc aaa gag gca g aggtatatta ttccattcat        13744
Glu Phe Glu Glu Glu Cys Lys Glu Ala
    1455                1460


ctgacttttt tttttttttt ttaaatttaa atttcaccaa attaattac ag gct ctt   13801
                                                         Glu Ala Leu
                                                             1465


atc gac caa aaa cgc gaa gaa tgg gac aaa aat ctc aac gat acc gcc    13849
Ile Asp Gln Lys Arg Glu Glu Trp Asp Lys Asn Leu Asn Asp Thr Ala
             1470              1475              1480


gtc att gac ctc gac gat tcg gat agt ctg ctg ctc aac gat cct tcg    13897
Val Ile Asp Leu Asp Asp Ser Asp Ser Leu Leu Leu Asn Asp Pro Ser
         1485              1490              1495


act tct gcc gat ttt tat cag agc tca agt ctt tta gac g aggtacgcga   13947
Thr Ser Ala Asp Phe Tyr Gln Ser Ser Ser Leu Leu Asp
        1500              1505              1510


tcgtcgtcgt cgcagcagca gccttctcca aaaagccgct caaaaaccgg caaaaaagcc  14007
tcaaaacttc caaattcgtg ctcgctcccc gtctaagcgt aaatctcagg ctccttcctt  14067
cgatccatat gtttcgtacg caccgcacgc gctcgcttct cccccggatt ccccgcgtaa  14127
gagaagatca cgtggtgcgc gtagtttagg tagtggtggt ggtggtggtg gtggtagtag  14187
atctgttgga agacctgccc gccgatcagt gaagaaagaa gaatcagatg atgatgatga  14247
ggattattgc caagaagagg aagtgaagcg aaatccggca gaaaaggtcc cgccgaaaag  14307
aaaacgagtt gtgtttgtgg aacctccaga ggtgaagccg ccggagccga aaaaacgagt  14367
tgttgttcct gctccatcat catcatcatc agctctaact actcttccac aacaaggacc  14427
gctgatttcg ttgccaaaag ctgtgccagt tgtacctcgg ccccaacaac aagcaccacc  14487
acagctcatc aaaaagcacc agcagactct gatgcctgtg aaggtgctca agattagtgg  14547
tggtggtggt ggtactccag gaccatccag tgtatcgcca ggtccatcaa tcctccgaag  14607
aaccgttgtt ccaggcatag gcgctggtgg tgttggacgc ctaccgcttg tcagaatgcc  14667
tgttcgccct ccatttcctg gctcgcaagc tcctgctcca ccgctgagaa gtggtgttgc  14727
tccaacagct cctgcagcag ctccacgcca gttcgtcgtt ccgtcgtcga gagttcgagt  14787
tatcacgacg agaactccgg tcgccaccac catggtgcaa caacaacaaa gcccgagccc  14847
gttgatgttt ccagtccggg ttgtgcaaag gcccgggcca tctggaccac caccacctgg  14907
acctccagat cgcccaggat ttggaatcta tgagaagccg agattctcac ttggatcacg  14967
aagaagccgt ggagattcgg gcccggaaga tccggcgcca ccacagccac caccacccac  15027
cacttctagg ccaccgccac aagcctaggc gctaggattt tccttttttt tttgttgatt  15087
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tttcgaaaaa aaaaacgaag aaagtttcaa attttttagct ttttttcaaaa aatcgaaaat 15507
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ttcttgaaat tatctgaaaa ccggaatttt ttttcaaaat tcgccatttt ttgcgaattt  15627
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aaattttttgt gatttttcga tttttttcac tccaaaaaaa ttccacacag caaaaaataa  15867
actccgcgca tttttgagcg caccttttcaa tgtttttaatt cttatcacga cgtcaaaatt 15927
cggttatttt tcacacacac acattttcct cccgagcggt tctttttttc atgagttctc  15987
ccatgttttg tttttatatt tgagacatttt tttttttgttg ataagtttca acttcttctt 16047
```

Fig. 19K

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```
cttcttctga ctataaacgt ttttctccat gttttttgcc tgttttctgc cgattttttg 16107
acacccaaaa ttttttttca ttttcgctcg aaaatgcacg tcgttggctc tagctttggc 16167
aagttttaa cactgatttt ctggtttttt ttttttttg cagaattttt cagagatagg 16227
gggctcattc cagcagggtt tcccactata tttcgcattt tttccaaaaa ttttgtatt 16287
ttcaaaaatt tccaaaaaga aaggggtttt ctttaccaaa ttttctcgc cacttttggc 16347
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gtttgatgtt tgacccccta ctatagaaaa tttgaaaaaa aaaaaaaaa aaaaaaacta 16467
gacgaaattt gtggaaatct tgctggagtt tgacgagtcg atggtggatt tttcttgaaa 16527
cgaatgaaac ggtgattttg gatcggagaa atatggcgaa aaatggtgag aaatgacgag 16587
gaggaggaag aagctgaaaa tctggaggaa caaaaattgt gtggaagtct cgggaagaaa 16647
ttagaattga aatttttaaag tgttctgaga atttttttgtg tgaaatttttt ttaaatctgt 16707
agatcaaata tcaaaaaaaa aaatcagaac tattacgtgt ttatccacaa agatgagaaa 16767
aatcgccata tctggcgcgc aaatgaaccc gcgggaagag acaaaactac tgtagttttt 16827
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aaaaaatttt ttttaaaaat tgcggctcaa aattaaattc aattcgatga cgcaatagct 17007
cgtaaatcta cacaaattgg ttaaaaacta cagtagtttt gtctcttccc gcgggttcat 17067
ttgcgcgcca gatatggtga tttttctcat ctctggataa acacgtaata acatttctcg 17127
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tagctttggg ccatttttggg ccgaaaaagc aaagtctcaa atttcagcac tccaactttta 17907
gcctttacct tggtgaaatt ttttaatctg tagtatactt tattttttggc cgacttttttg 17967
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ccggaacatt tgattttctg gaatataccg atttgccgga attttttggtt ttcggaaatt 18387
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tttccggcaa tatgccgatt tgccggaatt tttgatttcc ggcaatatgc cgatttgccg 18567
gaaattttga ttttcggcaa tataccgatt tgccggaaca tttggtttcc ggcaatatgc 18627
cgatttgccg gaattttttgg ttttcggaaa tttgccggaa atttagaatt ccggcaattt 18687
gccgatttgc cggaaatttt gatttccggc aatatgccga tttgccggaa attttggttt 18747
tcggaaattt gccggaaatt tagaattccg gcaatatgcc gatttgccgg aaattttgat 18807
ttccggcaat atgccgattt gtcagaagaa atcgtttgtc acccacgt gtattgattt 18867
gattttttct ag ata aaa ttc tac gac gag ctg gac gat atc atg cca atc 18917
                Glu Ile Lys Phe Tyr Asp Glu Leu Asp Asp Ile Met Pro Ile
                          1515                     1520

tgg ctt cca cca tca cca cca gat tcg gat gcg gat ttc gac ttg aga  18965
Trp Leu Pro Pro Ser Pro Pro Asp Ser Asp Ala Asp Phe Asp Leu Arg
1525           1530               1535               1540
```

Fig. 19L

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```
atg gaa gat gat tgt ctc gat ctg atg tat gaa att gaa caa atg aac   19013
Met Glu Asp Asp Cys Leu Asp Leu Met Tyr Glu Ile Glu Gln Met Asn
            1545                1550                1555

gag gct cgc cta cca caa gtt tgt cat gaa atg aga cgt ccg ttg gct   19061
Glu Ala Arg Leu Pro Gln Val Cys His Glu Met Arg Arg Pro Leu Ala
            1560                1565                1570

gaa aaa cag cag aaa cag aac acg ttg aat gcg ttt aa tggtaatatt     19109
Glu Lys Gln Gln Lys Gln Asn Thr Leu Asn Ala Phe Lys
        1575                1580                1585

ttcaaaaaaa aattttttg aaaaaattca attaaattcg attttgagca atttttatcg  19169
tgaagattgc ataattttga gattttgcgc caagattttt gttaaattga aaaaaagaga  19229
tgtgcgcctt tatggagtac tgtagttttg aaaattgaaa ttacagtact ctgtttaaag  19289
gcgcacacat gtattacgta gcgaaaagaa aagtacagta attagttaaa taagactact  19349
gtagcgcttg tgtcgattta cgggctctga attttatatg aattttgaa aactagaaac    19409
atctcaaatt gcataaaatt accatttgaa cctcccgcca agtgattttg ttcgacgggg  19469
cgcgcttgca cgttttctat tttaatttaa ttcaattttt tttgcttaat tctcaccgat  19529
ttttcatgtt ttcagtttga ttttgatgga aatttggaga caatatcaac ataaatgctt  19589
ttcaatcgaa aatgtgcatt tatattgaca ttttctccga atttccatca aaattaaact  19649
gaaaacacga aaaatcggtg agaattaagc gaaaaaattg agttaaatga aaatagaaaa  19709
cgtgcaagcg cgctccatcg aacaaaatca attggcggga ggttcaaatg ggaattgtat  19769
gcaattttca aaaggtcgta taaaatttttg aagaaagcaa attaaattta aaaaatcgag  19829
ctcgtaaatc gacacaggcg ctaattttca aaaaaataaa atgacaccca aaaaatcata  19889
agaaaatcat aaataaatat tacgggaaca caaaactcag agaacccgta ttgcacaaca  19949
tatttgacgc gcaaaatatg aaatatctcg tagcgaaaag aaaactaccg taatttaaaa  20009
acatttaaat gactactgta gcgcttgtgt cgatttacga gatctcgatt ttctaaataa  20069
attttttaaa aaatgatgtc agcgatattc catttgactt tgtttcttcg tattattttc  20129
tcattttgc ttgatttat ttaattttat aattttattt aaaatcaagc aaaaacgaga    20189
aaataatacg aagaaacgga gttaaatgga atatcgctga cataatttaa aaaaaaatt   20249
taattagaaa atcgagatcc cgtaaatcga cacaagtagt catagtacag tagtcattta  20309
actaattact gtacttttct tttcgctgcg agatatttca tattttattt catattttta  20369
tttattttca tattttata tatatatata tatatatatt tcttggcgtt ctaatgcagt    20429
ttctctcaat taattcc a gac att cta tcg gca aaa gaa aag gaa tcg gtg   20480
                     Asp Ile Leu Ser Ala Lys Glu Lys Glu Ser Val
                             1590                1595

tac gat gcg gtc aac aag tgc ctt caa atg cca caa tcc gaa gcg atc   20528
Tyr Asp Ala Val Asn Lys Cys Leu Gln Met Pro Gln Ser Glu Ala Ile
            1600                1605                1610

aca gca gaa tct gca gcg tct cca gca tac acg gaa cac tca tca ttc   20576
Thr Ala Glu Ser Ala Ala Ser Pro Ala Tyr Thr Glu His Ser Ser Phe
            1615                1620                1625

tcg atg gat gat aca agc cag gat gcg aag att gag cca agt ttg act   20624
Ser Met Asp Asp Thr Ser Gln Asp Ala Lys Ile Glu Pro Ser Leu Thr
        1630                1635                1640

gaa aat caa caa ccc acc acc acc gcc act act act act aca gta ccc   20672
Glu Asn Gln Gln Pro Thr Thr Thr Ala Thr Thr Thr Thr Thr Val Pro
1645                1650                1655                1660
```

Fig.19M

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```
caa caa caa caa caa cag cag cag caa aaa tcg tcg aaa aag aag aga   20720
Gln Gln Gln Gln Gln Gln Gln Gln Gln Lys Ser Ser Lys Lys Lys Arg
            1665            1670            1675

aat gat aat cga a cggtacggag gttactagcg aacaatttca agaaattttg   20773
Asn Asp Asn Arg
            1680

aatttgtgaa aattcaattc cggcaatttt tcgatttgcc ggaactttta attttcgccg 20833
aattgtcaat ttgccggaaa ttttgatttc cgccgaattg tcgatttgcc ggaacttttc 20893
attttcggca aattttcgat ttgccggaac ttttaatttt tgacaaattg tcgatgtgcc 20953
ggaaattttg attttcgaca atttgctgat ttgccggaaa tttcaatccc aacaattttc 21013
cgatttgccg gaaatttcaa tcccaacaat tttccgattt gccggaaatt tcaatcccaa 21073
caattttccg atttgccgga aatttcaatc ccaacaattt tccgatttgc cggaaatttc 21133
aatcccagca attttccgat ttgccggaaa tttcaattcc ggcaattttt cgatttgccg 21193
gaacttttca ttttcggcaa agtgtcgatt tgccggaact tttcattttc gccgaattgt 21253
cgatttgccc gaacttttaa tttttgacaa attgtcgttt tgctggaaat tttgattttc 21313
gacaatttgc caatttgccg gaacttttaa tttttgacaa attgtcgatt tgccggaaat 21373
tttgattttc gacaatttgc caatttgccg gaacttttca tttttgccaa attgtcgatt 21433
tgccggaaat tttaattccg gcaatttgc gatttgccgg aaatttcaat ccggcaatt 21493
taaaaacact aaaaaccaaa aattttcggt tttcccgttt ttcgatgttt cagcttttct 21553
caaaaaattg cgattccccg aaaaatcgaa acaattttcg gggttaaaac cgggaaattc 21613
ctaaattcct atttaaaaga attgaaaaaa aactctcaaa attcc ag gct caa aat 21669
                                                     Lys Ala Gln Asn

cga aca gct gaa aat ggt gtg aaa cga gcg aca act cca cca cca tca   21717
Arg Thr Ala Glu Asn Gly Val Lys Arg Ala Thr Thr Pro Pro Pro Ser
1685            1690            1695            1700

tgg cgt gaa gag cca gat tat gat gga gcc gaa tgg aat ata gtt gaa   21765
Trp Arg Glu Glu Pro Asp Tyr Asp Gly Ala Glu Trp Asn Ile Val Glu
                1705            1710            1715

gat tat gca cta ctt caa gca gtt caa gtc gaa ttt gca aat gct cat   21813
Asp Tyr Ala Leu Leu Gln Ala Val Gln Val Glu Phe Ala Asn Ala His
            1720            1725            1730

tta gtc gaa aaa tcg gcg aat gag gga atg gtg ttg aac tgg gaa ttc   21861
Leu Val Glu Lys Ser Ala Asn Glu Gly Met Val Leu Asn Trp Glu Phe
            1735            1740            1745

gtg tcg aat gcc gtt aat aag cag aca aga ttt ttc cgc tcg gcc cgt   21909
Val Ser Asn Ala Val Asn Lys Gln Thr Arg Phe Phe Arg Ser Ala Arg
        1750            1755            1760

caa tgc tca att cga tat caa atg ttt gtt cgg cca aaa gag ctc gga   21957
Gln Cys Ser Ile Arg Tyr Gln Met Phe Val Arg Pro Lys Glu Leu Gly
1765                1770            1775                1780

cag ttg gtg gct tct gat ccg att tcc aag aaa acg atg aaa gtc gac   22005
Gln Leu Val Ala Ser Asp Pro Ile Ser Lys Lys Thr Met Lys Val Asp
                1785            1790            1795

cta tcg cat act gaa tta tct cat ttg aga aaa gga cga atg act acg   22053
Leu Ser His Thr Glu Leu Ser His Leu Arg Lys Gly Arg Met Thr Thr
            1800            1805            1810
```

Fig. 19N

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```
gag agc caa tat gct cat gat tat gga ata ttg act gat aag aaa cat   22101
Glu Ser Gln Tyr Ala His Asp Tyr Gly Ile Leu Thr Asp Lys Lys His
        1815            1820            1825

gtg aat aga ttt aaa agt gtt cga gtg gcg gca aca cgg aga cct gtt   22149
Val Asn Arg Phe Lys Ser Val Arg Val Ala Ala Thr Arg Arg Pro Val
        1830            1835            1840

cag ttt tgg aga ggc cct aaa ggt aga gga gga tgg ctt cat aat agt   22197
Gln Phe Trp Arg Gly Pro Lys Gly Arg Gly Gly Trp Leu His Asn Ser
1845            1850            1855            1860

cac tgc aac ttt ttc ctc acg agg gac gag aaa aag tgg ttt cta ggc   22245
His Cys Asn Phe Phe Leu Thr Arg Asp Glu Lys Lys Trp Phe Leu Gly
            1865            1870            1875

cat ggc cga ggt gcc gac aag ttt ca gcggccattt atcttgcttt          22291
His Gly Arg Gly Ala Asp Lys Phe
            1880

gttttccgcc cgttttcttt cgtttttcac cgattttttt cgttttttct taataaaact 22351
gataaataaa tatttttttgc agatgctaaa aaaatttcca agtaaaaaaa tcatgtattc 22411
agtgggcatg cagcggtgaa agtgggcatt gtaatatgat ggattacggg tatacaaaac 22471
ctaaactttt tctgaaacat gatacatgtg ctgcttaaat gctgagacta cctgattttc 22531
ataacgagac cgctgaaaaa gttttgaggt ttccaaaatt caactttttt ggtgaaaaag 22591
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Fig. 19O

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Fig. 19P

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Fig. 19Q

Title: RB PATHWAY AND CHROMATIN REMODELING
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Fig. 19R

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caccacaatc ctttaagttc cctctgacaa tgagctcatt atacatgtgt aaaaagccgc 36271
catcacagga aaattccagt ttcggattat tctcgattct aatatcacac gcctcgatac 36331
cccgatcacg gtacaagtag agatcgtaga gcacactggg gtcgtttaat tgtgaattgt 36391
ttcggatgta aacaccgtct gaaatctgaa gtttaagaaa aaattaagta agttttaatc 36451
tacatgttga tccgtttttg ttgaaagtat caaaaaatta actggagtca gaatgtctca 36511
tttcgttttg atcttcaaaa aatgcgggag ttcagaccta gacatctcgt ctgatttcgc 36571
atggttaaga gcgttctgac gtcacaattt ttctgaaaaa atattcccgc atttttttgta 36631
gatcaaatta aaatgagaca gcctgacacc acgtggagtt ccttatatac aaaaaagttg 36691
attttttcgct cgtgattttt cgttgtaaca tcatgaaaaa tccagtgttc tctgcaaacc 36751
actaaaatcc acttttttgt ttcagccgct ccgcaagcag cttcgtcgag gtcatggcag 36811
cggccgagtt tcccactccg ctgaaactcg gcacttaata tatgaacgac taagctagca 36871
gggccgccat tctaccttac cagcaaaaat gaattcgttc acttacacac atcacacacc 36931
acattaaagt ttcctttttc tttgtcagct gtaaaaaccg aaaggcttgt cagactagta 36991
ttctcaatat taaatc                                                  37007
```

Fig. 19S

Title: RB PATHWAY AND CHROMATIN REMODELING
GENES THAT ANTAGONIZE *LET-60* RAS SIGNALING
Applicant(s):Horvitz *et al.*
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lin-65 genomic sequence (1 kb of upstream and downstream genomic sequence is included in this file)

Exon number	Exon boundaries (inclusive)
1	1001 - 1133
2	4522 - 5208
3	6128 - 6361
4	7962 - 8350
5	8706 - 8928
6	9260 - 9516
7	10328 - 10567
8	11677 - 11700

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AAAAATTTAAAAAAATTTTTAAAAATTCGTGTAAAAATTACCCCGGTTGTTTAGGAA
ATAATAAAGAGATTAGAGACTTTTTTCAGATTTTTATTTTCTTGAGTTTTGCCGGTT
TTCAGCCGATTTCTATCTTTTTTTTCTCATTTTTTGTGATTTTTTTTCGCTAGTTTT
CCCCTCAATTTCTCGATTTTTTCACGATTTTTTGAAAATTTTCGGAAAATTGAATTG
TTTGCAAAAAAAAAATTCAAAAACCGCATTTTTCTCAGAATTTTTCTGGGATTTTG
TACAAATTTTTGAATTATTTCTCAAAAAAAAGCAGGTTTTTACCGATTTTTTTGGTT
TTTTCCCCAAAATTTTCCGATTTTTTCCGAGTTTTGCCGGTTTTCAGCCGAATTCTA
CTCTCGATTTTTTTACGATTTTTTGGAAATTTTCGGAAAATTATTTGAAAAAAAATC
AAAAAACCGCATTTTTTTTTCTGAATTTTCTGGGATTTTGTACGAAATTTTGAAATT
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TTCTCGAAATTTGCACAAAATTTTTGAATTTTTTCGTAAAAAAAAACTGTTTTCCCC
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CTTAAATACAGAAGCTTCAGATGATCCAATACCTCCATTAAATGATGATCAGATTGC
TGAGCTTTTGGGTGAAGATGGAGAAATTATGGAGATAACTGAGCAGAAGGTGAGAT
TTTTTGAGTAAAACCTTGAATTTTGCACTAAAAATTTGCAATTTTCGCTAAAAATTA
CCTTAAAACTCGAAAATTGGAATTTCTAGCTGAGAAAATGGCCAAAAATGTCGAAAA
```

Fig. 27A

Title: RB PATHWAY AND CHROMATIN REMODELING
GENES THAT ANTAGONIZE *LET-60* RAS SIGNALING
Applicant(s):Horvitz *et al.*
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```
ATGCCTCCGAAACCTGTGAAAAAAAAAACCACCAAAAAGGTTTCTAGGCCACCAAAAA
GATTTCTAGGCCACCAAAAATGTTTCTAGGCCACCAAAAATGTTTCTAGGCCACCAAA
AATGTTTCTAGGCCACCAAAAATGTTTCTAGGCCACCAAAAATGTTTCTAGGCCACCA
AACAGGTTTCAATGCCACCAAAAATGTTTCTAGGCCACCAAAAATGTTTCTAGGCCCC
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GCCACCAACCAGGTTTCAATGCCACCAAAAATGTTTCTAGGCCACCAAAAAGGTTTCT
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CACCAAAAATGTTTCTAGGCCACCAAAAATGTTTCTAGGCCCCCAAAAAATTTTTCTA
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GCCACCAAACAGGTTTCAATGCCACCAAAAAGGTTTCTAGGCCACCAAACAGGTTTCA
ATGCCACCAAAAATGTTTCTAGGCCACCAAAAAGGTTTCTAGGCCACCAAAAATGTTT
CTAGGCCACCAAAAATGTTTCTAGGCCACCAAAAAGGTTTCTAGGCCACCAAAC
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Fig. 27B

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GENES THAT ANTAGONIZE *LET-60* RAS SIGNALING
Applicant(s):Horvitz *et al.*
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AGGTTTCAATGCCACCAAAAATGTTTCTAGGCCACCAAACAGGTTTCAATGCCCCCAA
AAAATTTTTCTAGGCCACCAAAAAGGTTTCTAGGCCACCAAAAATGTTTCTAGACCAC
CAAAAAGGTTTCTAGGCCACCAAAAATGTTTCTAGACCACCAAAAAGGTTTCTAGGCC
ACCAAAAATGTTTCTAGGCCACCAAAAAGGTTTCTAGGCCACCAAACAGGTTTCAATG
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GATGACGACACTCCGGAACCGATTCTCGTGATTGATATGGATGAGGATGAGGATGTTA
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TGCTCAGGATGTTCCGGATTCTTTGGGAGCTTCAGATGCTTCAGCTCAAGAAATTCCA
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TGCTCGCCGAGCAAAATGGAGTTTTGGACGAAGGATTTGATGAGACTGACGATATTAT
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TCAGAAAAAGCTAAAATTTTCCCAAAAAATCCCAGAAAAGCAGAATTTTCATTCAAA
ATTCCCAGAAAAAGCTGATAATTTACTAAACAATCTCAGAAAATGCTGAAATTT
```

Fig. 27C

Title: RB PATHWAY AND CHROMATIN REMODELING
GENES THAT ANTAGONIZE *LET-60* RAS SIGNALING
Applicant(s):Horvitz *et al.*
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TACTCAAAAGTCTTCATAAAAAGCTGAAATTTTACTTTAAAAGTTTAGGAAATGCTGC
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GCCACCAAAAAGGTTTCTAGGCCACCAAGAAAGTTTCTAGGCCACCAAAGTATTTATA
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```

Fig. 27D

Title: RB PATHWAY AND CHROMATIN REMODELING
GENES THAT ANTAGONIZE *LET-60* RAS SIGNALING
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TAGGCCACCAAAAAGGTTTCTAGACCACCTAAGACATTTCTAGGCCAACAAAAAGGTT
TCTAGGCCACCAAGAAGCCGAAAAACTGTCTCAAATTCGAATTTTGCAGTGCTCAAAC
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CCGTTCAGCATTGAAAGAATTGACTAATGAAATAACTGGAATGCGTGTACAAATGAAT
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AACGTCATCAGGCTTTCGAGCAGCAACAACAATTCCAACACCAACACCACCAACACCG
ACCAATAATGTTGGCTCCACGTCATCATCCGCCGCCGCCCCGCATTTTACACCGAAT
CAACGGGCGGCGGCTCCGTATCATCCGAATATGGTTCAACCGAATCGTCTTGCTGCTA
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CGGGCCGGAAAATTTTGGAAAATCCTCTAAATTTTCAATATTTGTCGAAAAAATCTGA
CAAAAATCGTGTCAAAATTCAGATTTCCGGGAGAAAAATCGCATTTTTGAGTAAAAAT
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TCAAGAAAATTAAGAAAAATGCGAAAATTTCGAGCAAAAAATATAGTTTTTTGGAGCC
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AAAACCACTTTTTTAAAAAAAATTTTCACACAATTTCCAGCAACAAAATTCGGCTCCAC
CACAATTCAACGGTCACCAAGCTCTCGTCCCATCACCTCAATCATCATCTGCATTTTC
TCGTCCACCACCAACTCAACTTGCAACACAGAGAAGAGCTCCACCATTGGCAAGTACC
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TGGAAATTAACAAAAACCAAATAAAATGCCCTAATTTTTTTTTAAATCCAAAAATTGT
TGGATTTTTTCAGAAAAAAATATTTTTTCAATTGACTGGTGTCCAAAAAATATAGAAA
ATTCAAATTTTCCAAGAAAAATAGCCAAAAAAATGTAATTTTTGTCTAACAAAAAAAT
TGAATAGCGCAAAATTAAATTGTCGTTTTTTTTAATTTCCCTCCGGTTTTGAAA

Fig. 27E

Title: RB PATHWAY AND CHROMATIN REMODELING
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ATTTGTTCAAAAATGGCAAAGTTTTCGAAATTTTAGTCTAAAAAAGATTTTTT
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AAATTCCTAAAAAATCAATTTTCAGTCAAAAATTAAATTT
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Fig. 27F